

P1748R1

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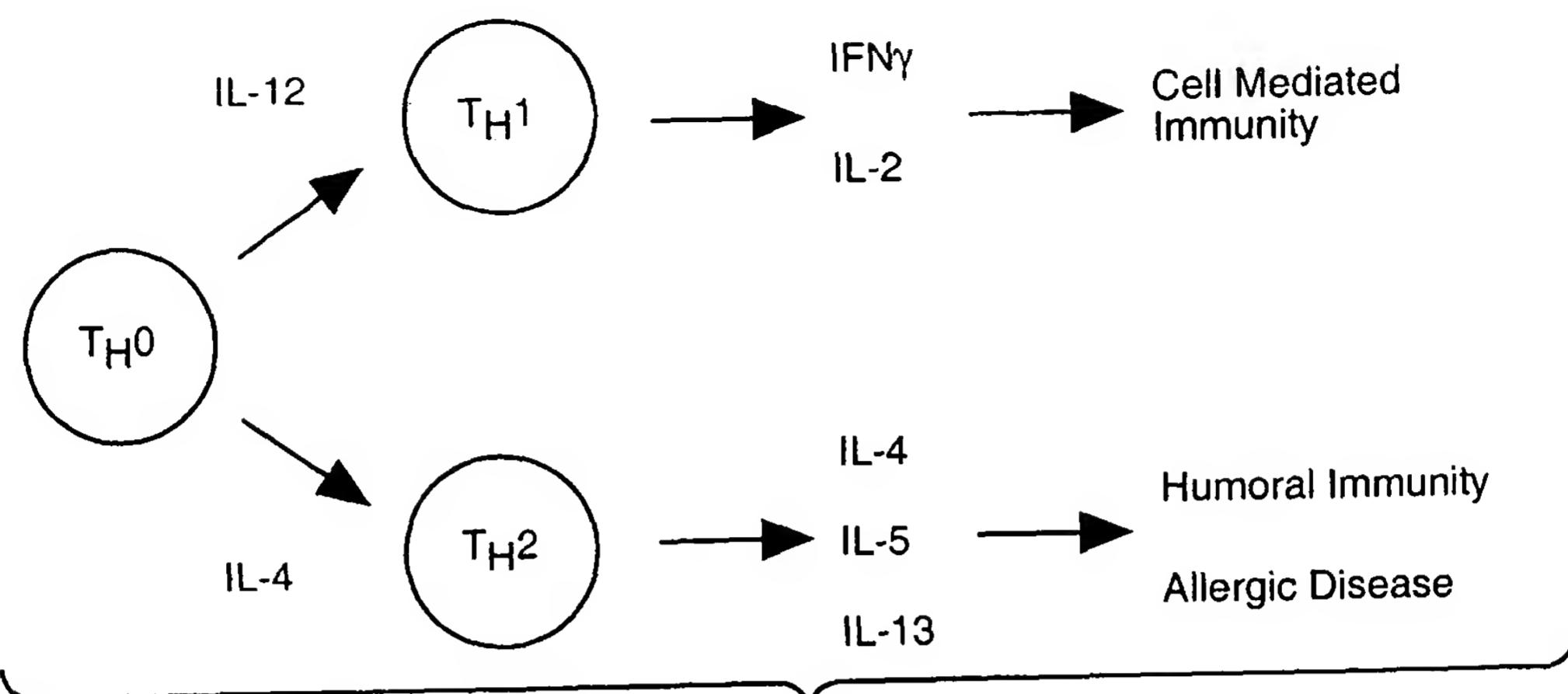


FIG._1

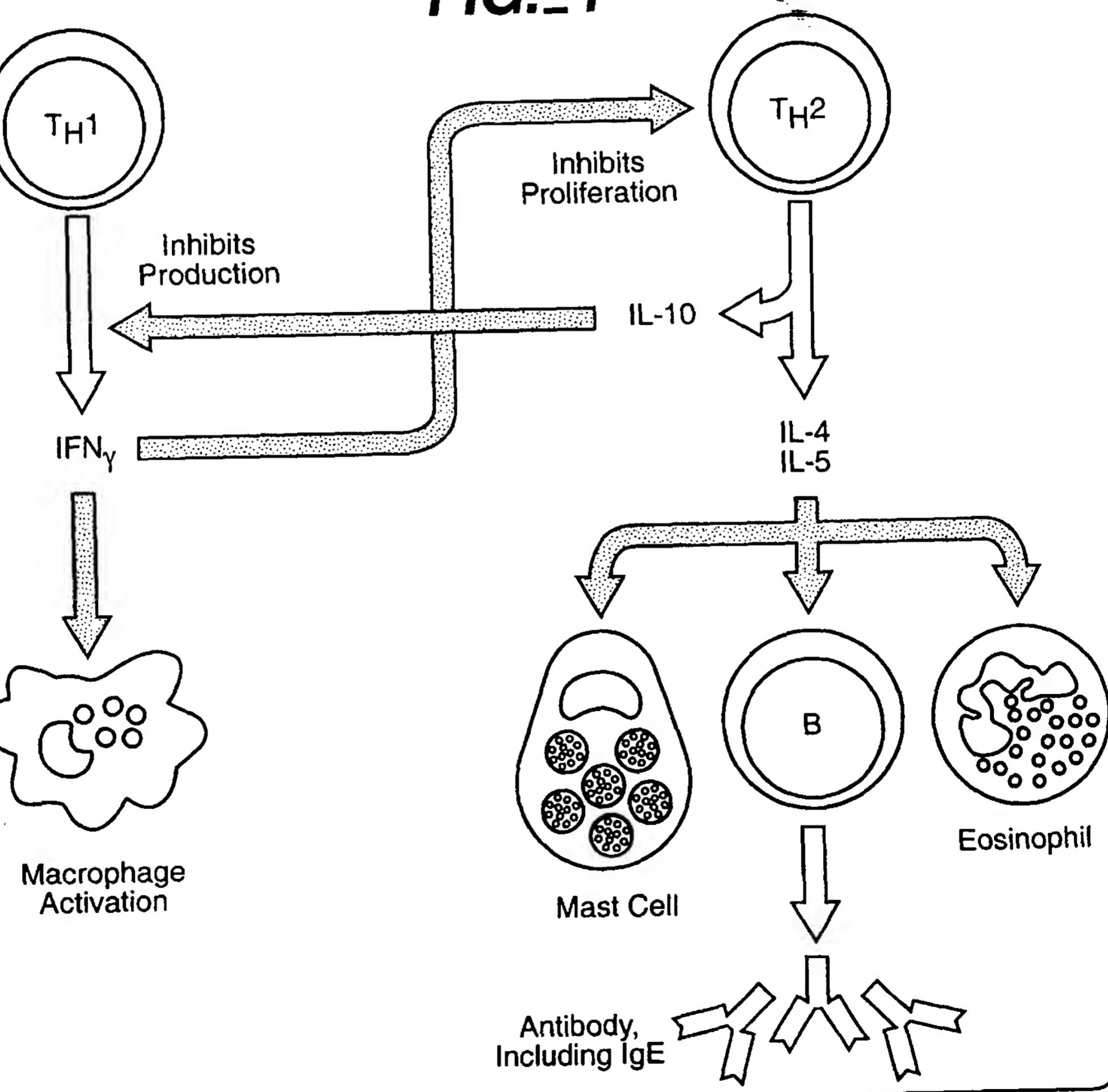


FIG._2

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MRGGRGAPFWLWPLPKLALLPLLWVLFQRTRPQGSAGPLQCYGVGPLGDLNCSWEPLGD
LGAPSELHLQSQKYRSNKTQTVAVAAGRWSVAIPREQLTMSDKLLVWGTKAGQPLWPPV
FVNLETQMKNAPRLGPDVDFSEDDPLEATVHWAPPWPSHKVLICQFHYRRCQEAAWT
LLEPELKTIPLTPVEIQDLELATGYKVYGRCRMKEEDLWGEWSPILSFQTTPSAPKDV
WVSGNLCGTPGGEPEPLLWKGPGPCVQSYKVWFVWGGRELSPEGITCCCSLIPSGAEW
ARVSAVNATSWEPLTNLSLVCLDSASAPRSVAVSSIAGSTELLVTWQPGPGEPLEHVVD
WARDGDPLEKLNWVRLPPGNLSALLPGNFTVGVPYRITVTAVSASGLASSVWGFREE
LAPLVGPTLWRLQDAPPGTPAIAWGEVPRHQLRGHLTHYTLCAQSGTSPSVCMNVSGNT
QSVTLPDLPWGPCELWVTASTIAGQQGPPGPILRLHLPDNTLRWKVLPGILFLWGLFLLG
CGLSLATSGRCYHLRKVLPRWVWEKVPDPANSSSGQPHMEQVPEAQPLGDLPILEVEE
MEPPPVMESSQPAQATAPLDGYEKHFLPTPEELGLLGPPRPQVLA

FIG._3

MNRLRVARLTPLELLSLMSLLLGRPHGSPGPLQCYSVGPLGILNCSWEPLGDLETPPV
LYHQSQKYHPNRVWEVKVPSKQSWVTIPREQFTMADKLLIWGTQKGRPLWSSSVNLETQ
MKPDTPQIFSQVDISEEATLEATVQWAPPVWPPQKALTQFRYKECQAEAWTRLEPQLKT
DGLTPVEMQNLEPGTCYQVSGRCQVENGYPWGEWSSPLSFQTPFLDPEDVVWVSGTCETS
GKRAALLVWKDPRPCVQVTYTWWFGAGDITTTQEEVPCCKSPVPAWMEWAVVSPGNSTSW
VPPTNLSLVCLAPESAPCDVGVSADGSPGIKVTKQGTRKPLEYVVDWAQDGDSLDKLN
WTRLPPGNLSTLLPGEFKGGVPYRITVTAVYSGGLAAAPS梧GFREELVPLAGPAVWRLP
DDPPGTPVVAWGEVPRHQLRGQATHYTFCIQSRLSTVCRNVSSQTQTATLPNLHGSFK
LWVTVSTVAGQQGPPGPDLSSLHLPDNRIRWKALPWFLSLWGLLLMGCGLSLASTRCLQARC
LHWRHKLLPQWIWERVPDPANSNSGQPYIKEVSLPQPPKDGPILEVEEVELQPVVESPKA
SAPIYSGYEKHFLPTPEELGLLV

FIG._4

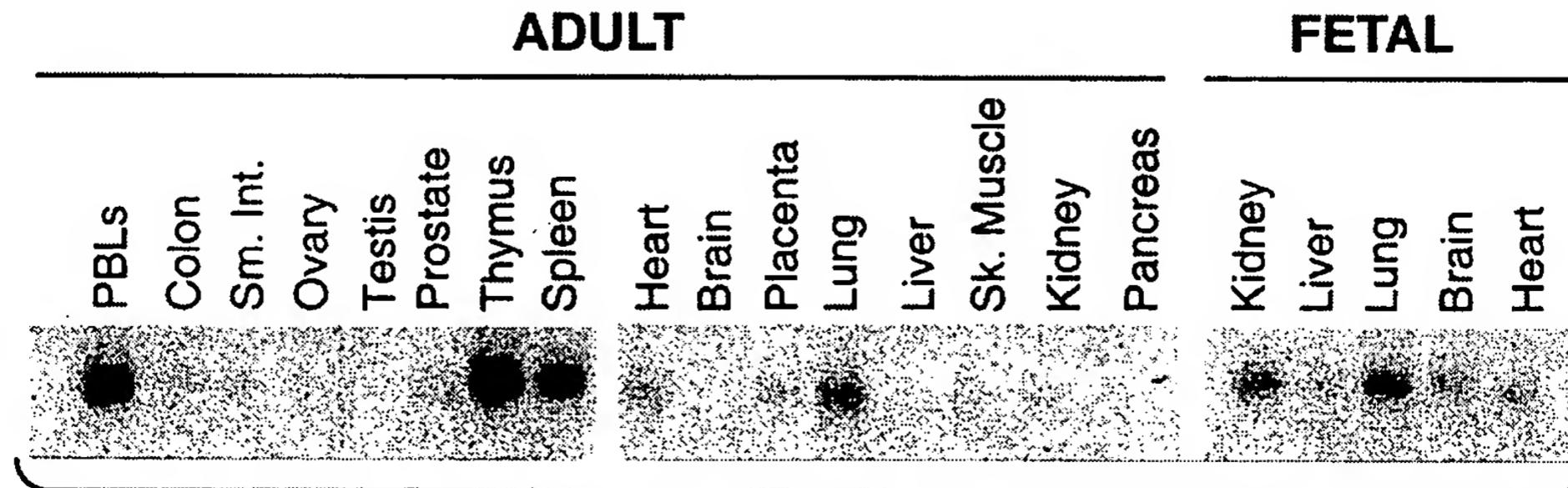


FIG._6

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| | | | |
|--------|-----|--|--------|
| h-TCCR | 1 | MRGGRGAPFWLWPTPKLAATPLIWWFQRTPQGSAGPLOCYGVGFLGDE | |
| m-TCCR | 1 | - - - MNRLRVARETPPLEELLSIMSELLGTRPHGSPGPLGIL | |
| h-TCCR | 51 | NCSWEPLGDLGAPSETHLQSQQKYRSNKTQTVAVAAGRSSWVAIPREQLTWS | |
| m-TCCR | 46 | NCSWEPLGDLGETPVEYHQSQKYYHPRNVRWEVKYPSKQSWTIPRFITMA | |
| h-TCCR | 101 | DKLLIVNGTAKAGQPIWWPPVNFVNLETQMKPNAAPRLGPDVDFSEDDPLEATH | |
| m-TCCR | 96 | DKLLIWGTQKGRMPTQVSYNLETQMKPDTPQIFSQVDITSEEAITLEATVQ | |
| h-TCCR | 151 | WAPPTWPSHKVTLICOFHYRCQEAAWTLEPELKTIPLTPVEIDDELAT | |
| m-TCCR | 146 | WAPPVWPPQKALTCCOFRYKECCAAWTLEPELKTIPLTPVEIDDELAT | |
| h-TCCR | 201 | GKKVYGRCRMEEKEEDLNGEWSPILSFQTPPSAPKDVNWVSGNLCGTPGGE | |
| m-TCCR | 195 | CXQVSGRCCQVENGYP-WGEWSPILSFQTPPSAPKDVNWVSGTVCETSGKRA | |
| h-TCCR | 251 | PLLWKAAPGPCVQSYKVKWFVGRELSPSEGITCCSLLIPSGAEWARYSA | |
| m-TCCR | 245 | ALLVWKDPRPCVQSYKVKWFVGRELSPSEGITCCSLLIPSGAEWARYSA | |
| h-TCCR | 301 | VNTSWEPLTNISLVCLDSASAPRSVAVASSIAGSTELLVTWQPGPEPLE | |
| m-TCCR | 295 | GNSTSWVPPPTNLSLVCLADESAPFCDVGVSSADGSPGIKVTMKQGTRKPE | |
| h-TCCR | 351 | HYVDWARDDGDPLEKENNWVRLPPCGNLSAALEPGNETVGVPYRITVTAWSASG | |
| m-TCCR | 345 | YVVDWAQDGDSSLDRKLNWTRLPPCGNLSAALEPGNETVGVPYRITVTAWSASG | |
| h-TCCR | 401 | YASASSVWGFREELAPLVGPPTLWRLQDAPPGTPTVVAWGEVPRHQLRGQA | |
| m-TCCR | 395 | YAAASSVWGFREELVPLAGPAVWRLLPDDPPGTPTVVAWGEVPRHQLRGQA | |
| h-TCCR | 451 | HYTLCAGSGTSPSVCMNVSGNTQSVTLPDIPWGPCEFWYTAASTIAGQQCPP | |
| m-TCCR | 445 | HYTFCIQSRGLSTVCRNVSQQTQATLPNLHSASFKLWVTVSTVAGQQCPP | |
| h-TCCR | 501 | GPIIRLHLPPDTLWRKVRPGLTLLGCCSWSATSGRCYHLR | |
| m-TCCR | 495 | GEPDLSHLPDNTRIRWKAIFPWFSSWGLLHEMCCGILSEASTRCLQARCLHWR | |
| h-TCCR | 547 | HKVLPKRWVWEKVPDPAASSSGOPHMEQVPEAOFLGDLPTILEVEEMEPVV | TM |
| m-TCCR | 545 | HKLPLPQWVWEKVPDPAASSSGOPHMEQVPEAOFLGDLPTILEVEEMEPVV | TM |
| h-TCCR | 597 | MESSQPAQATAAPLDSSGYERHFLPTPEELGIGPAPRQVLA | FIG.-5 |
| m-TCCR | 595 | YES - - - PKASAPIYSGYERHFLPTPEELGIGPAPRQVLA | |

Box 1

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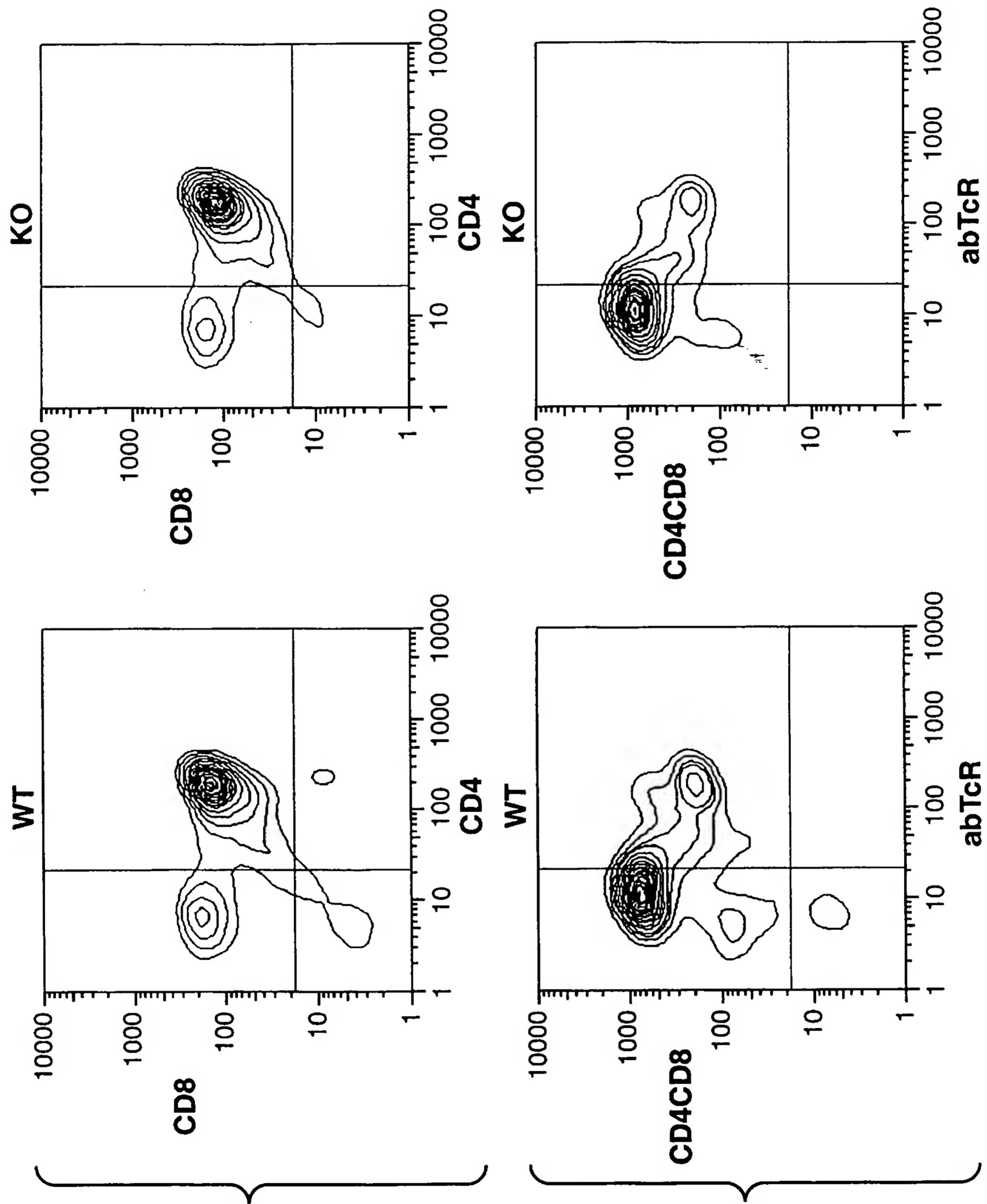


FIG.-7A

FIG.-7B

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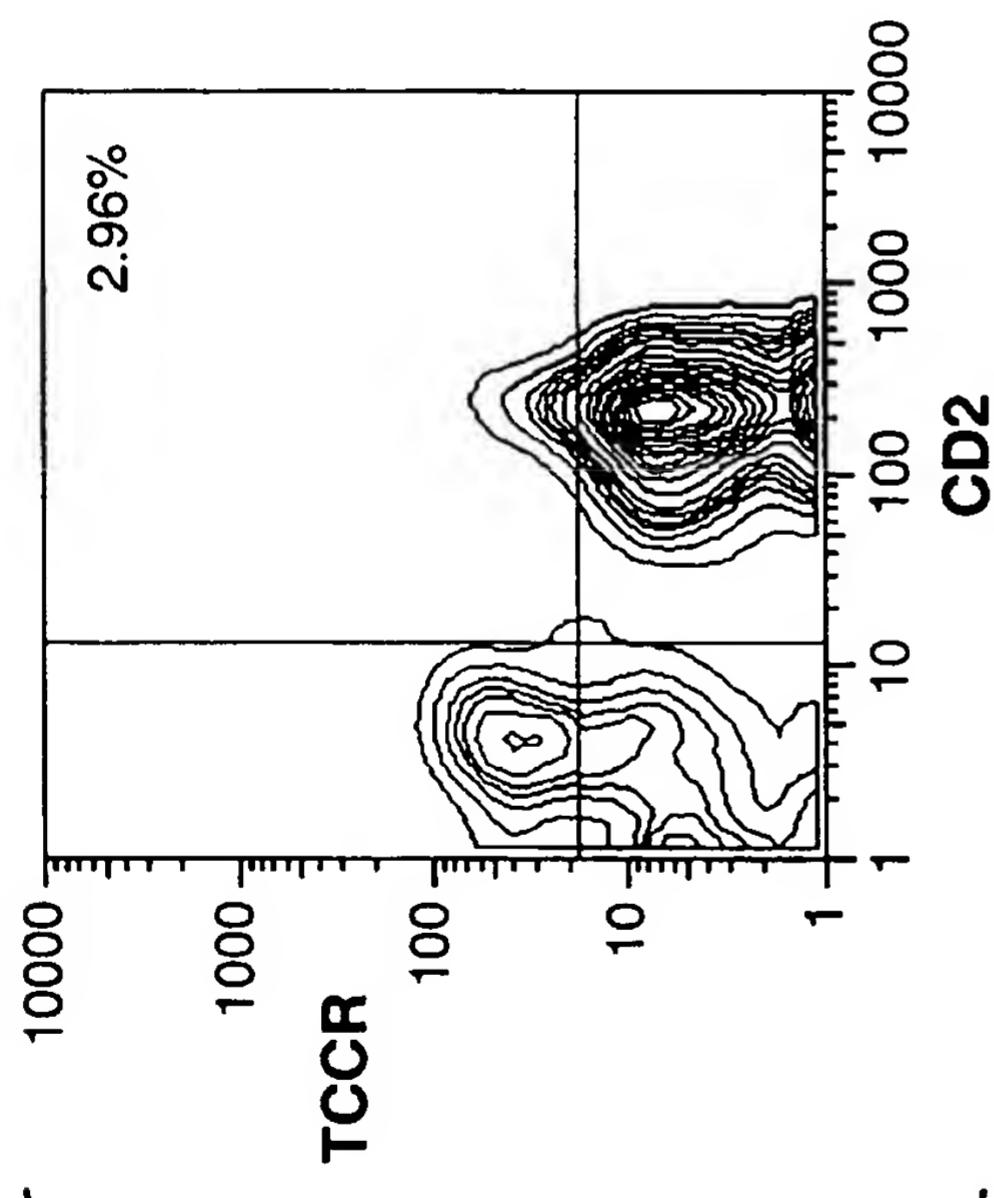
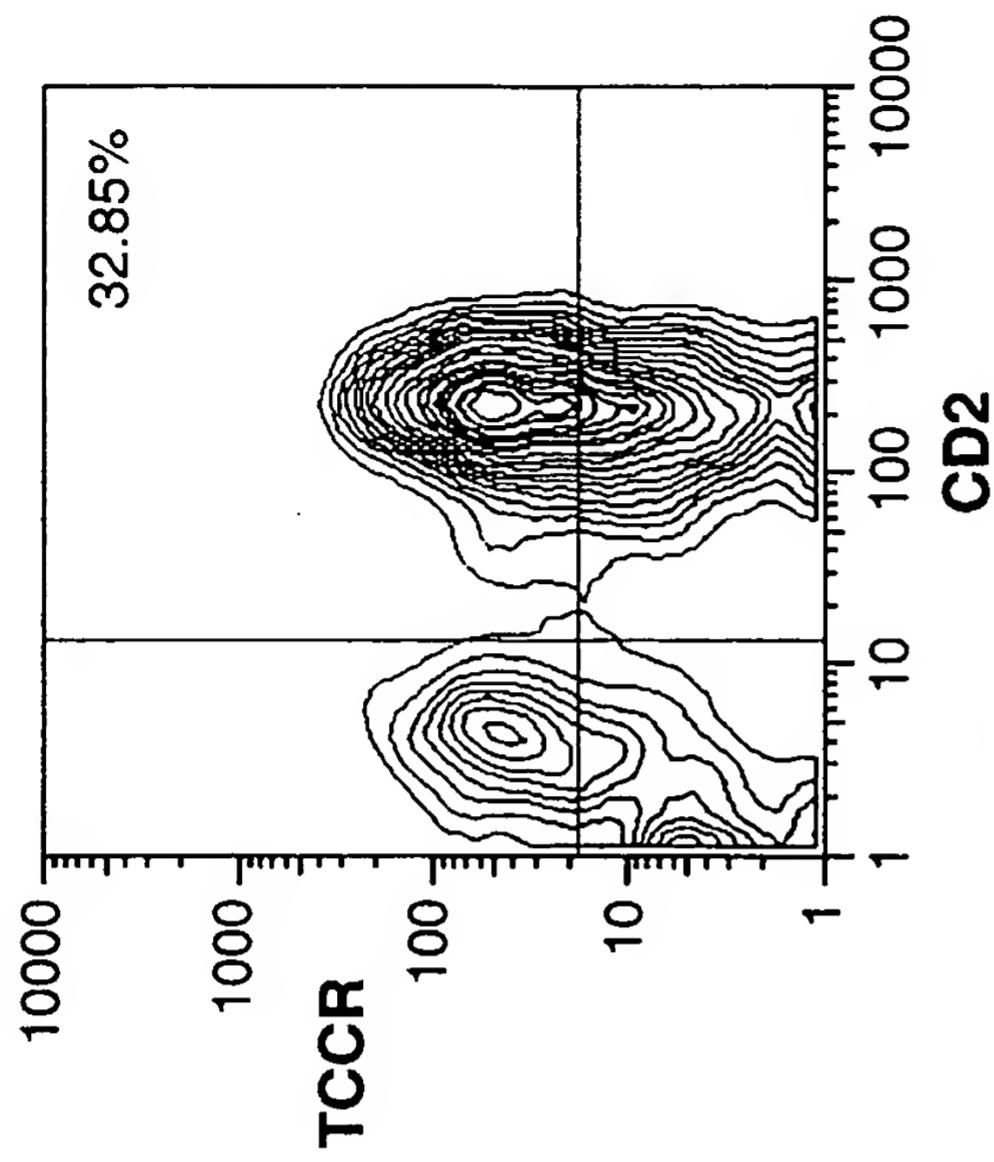


FIG._8A

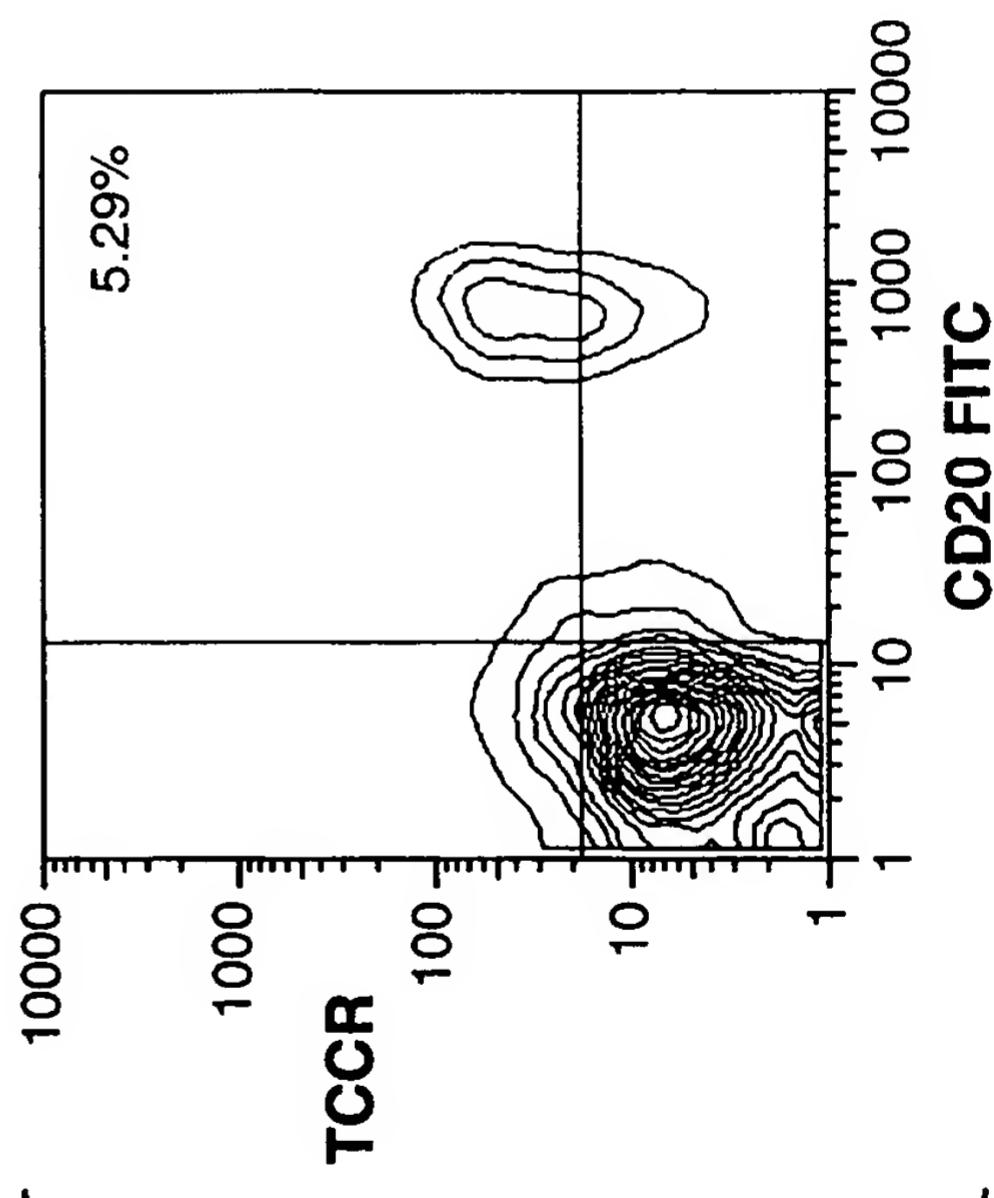
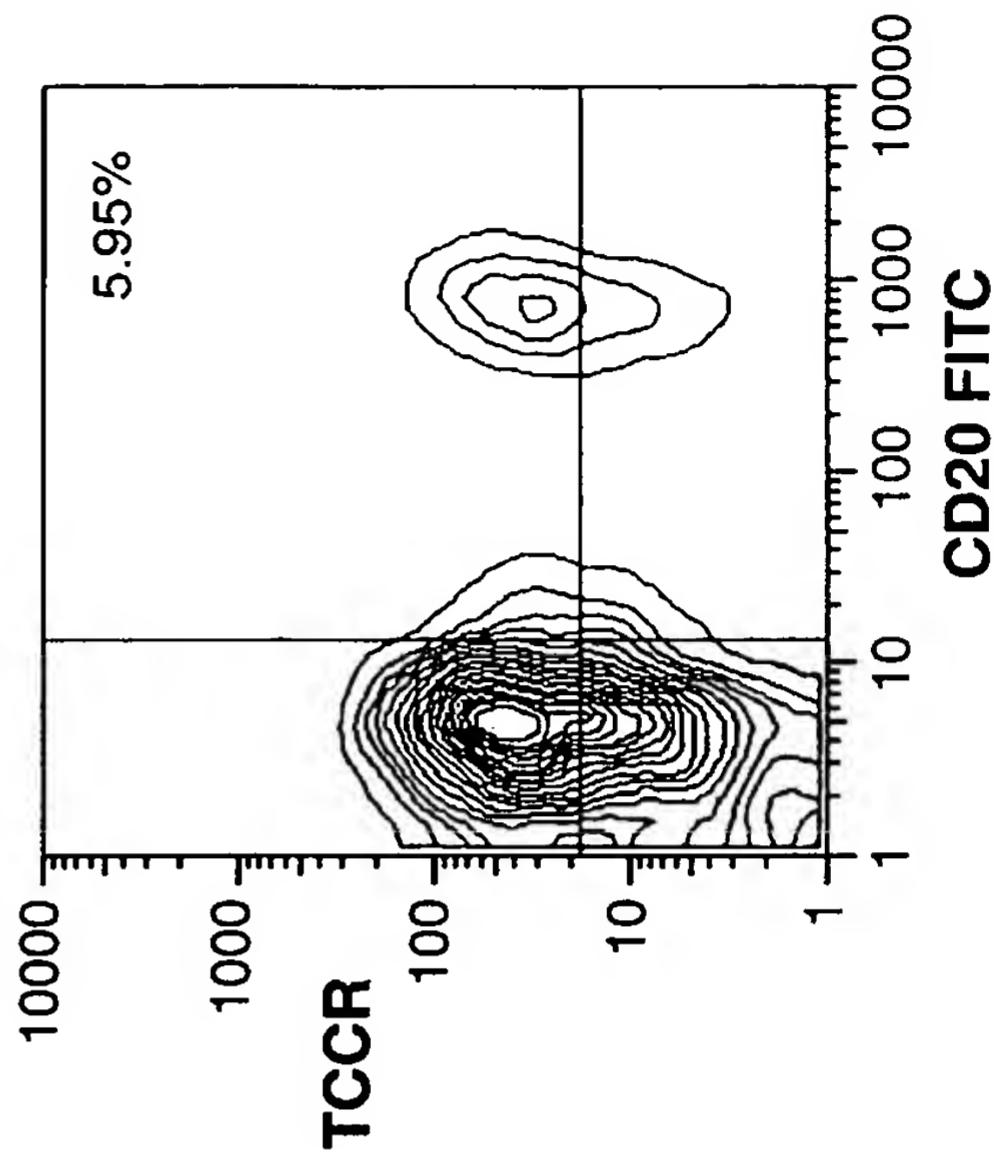
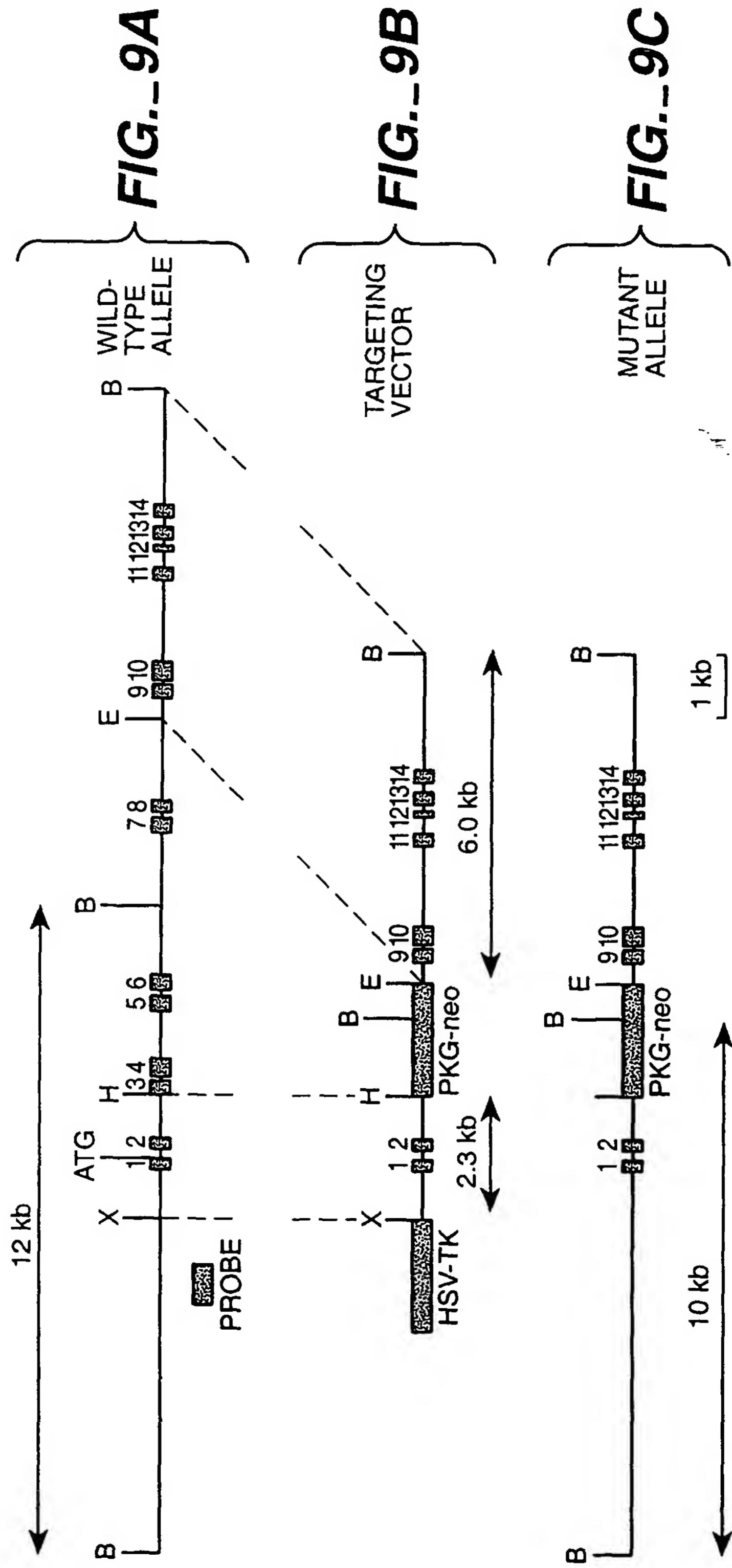


FIG._8B

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FIG._10A

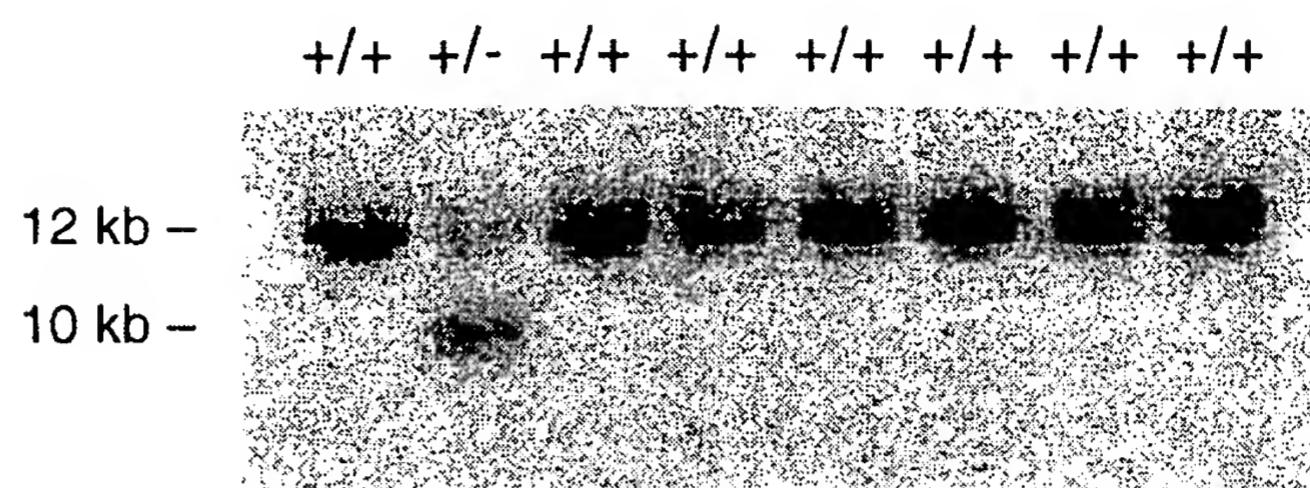


FIG. 10B

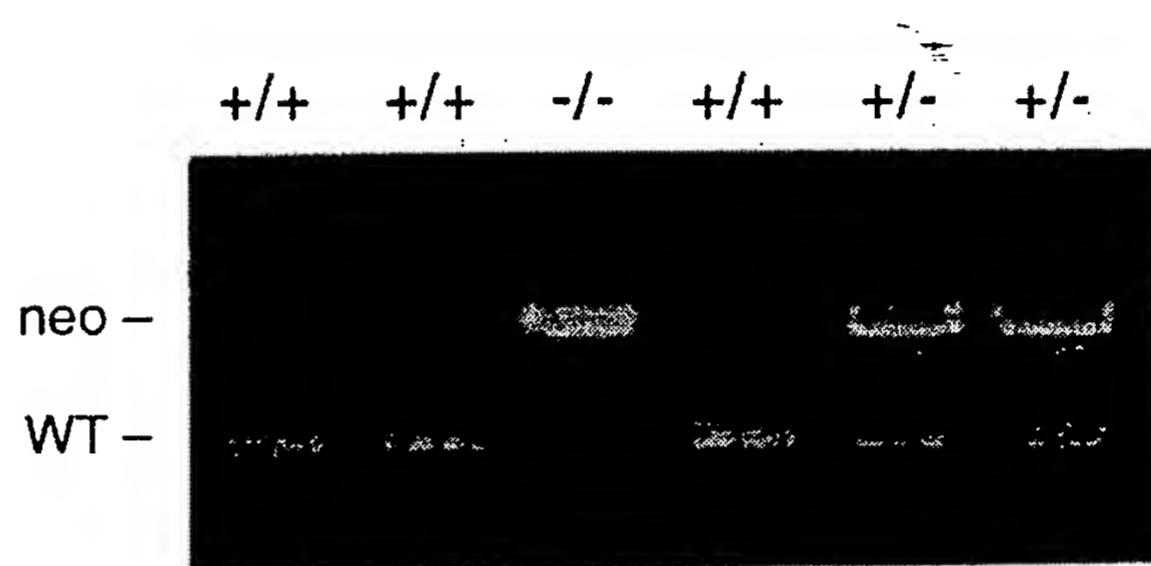
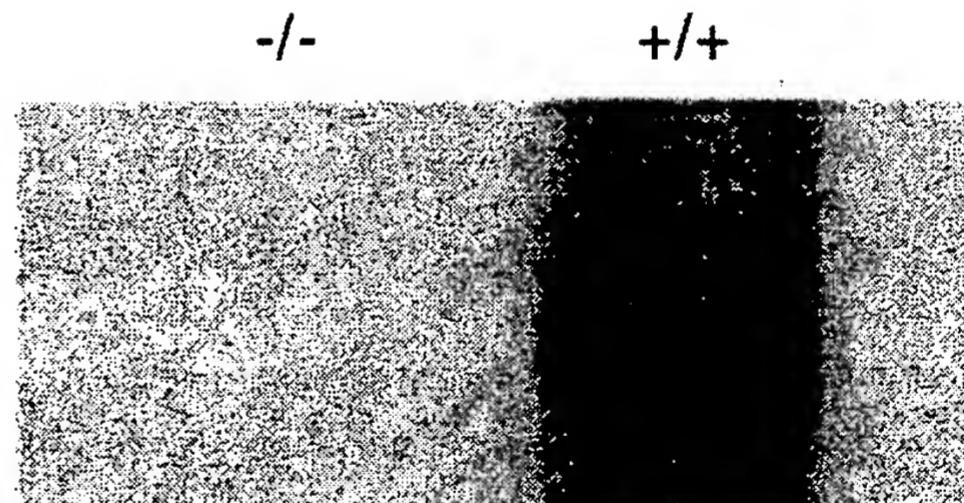


FIG._10C



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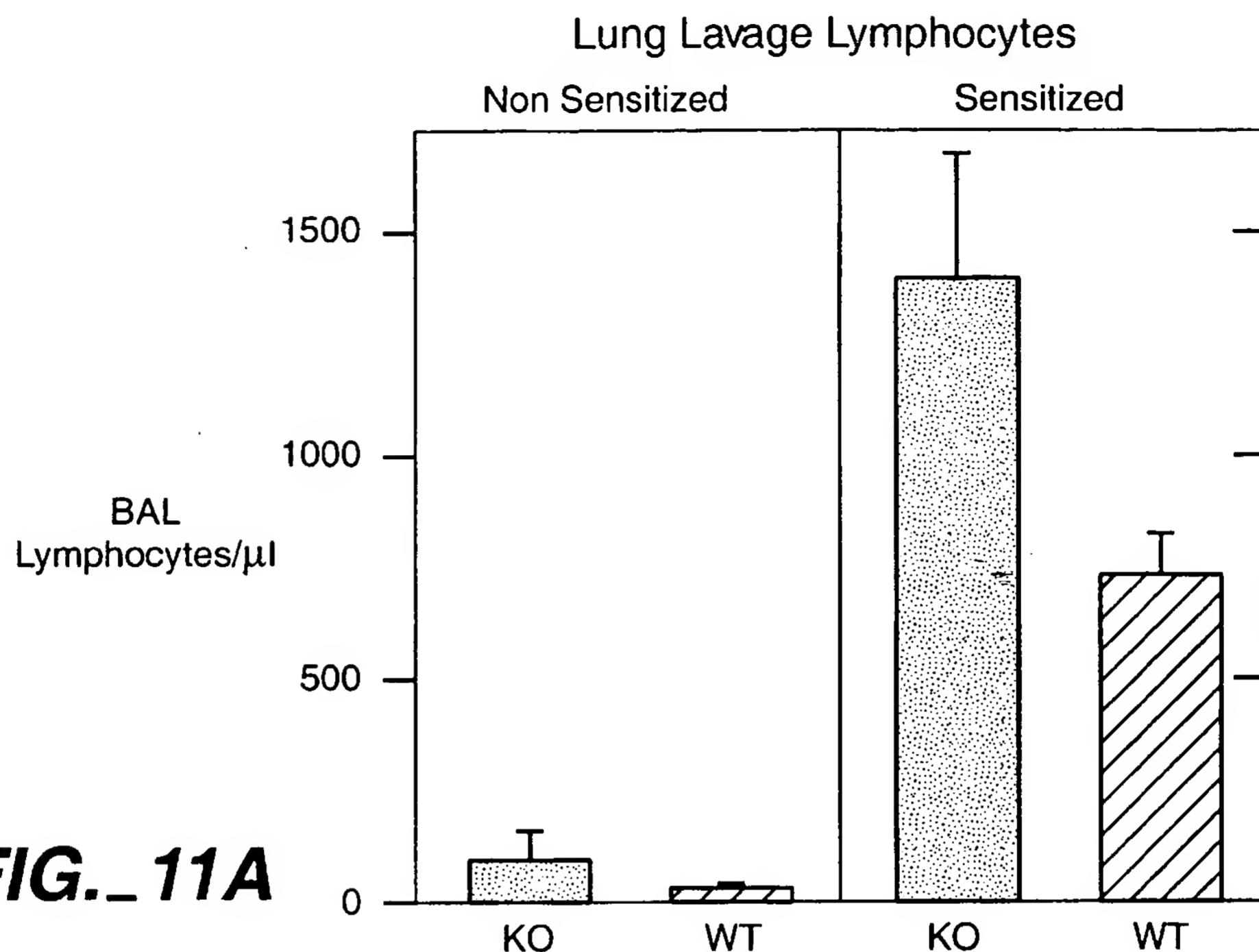


FIG._ 11A

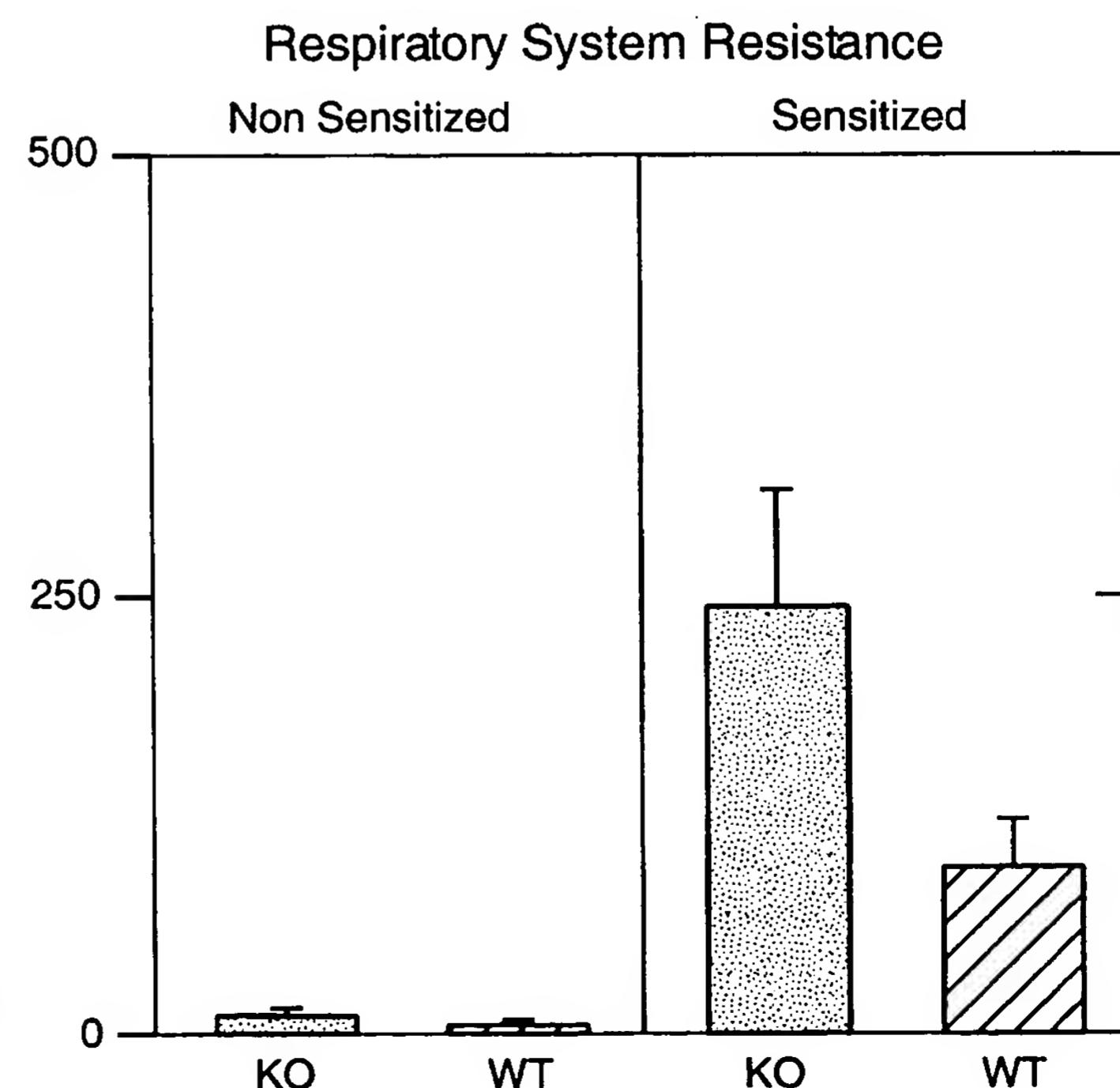


FIG._ 11B

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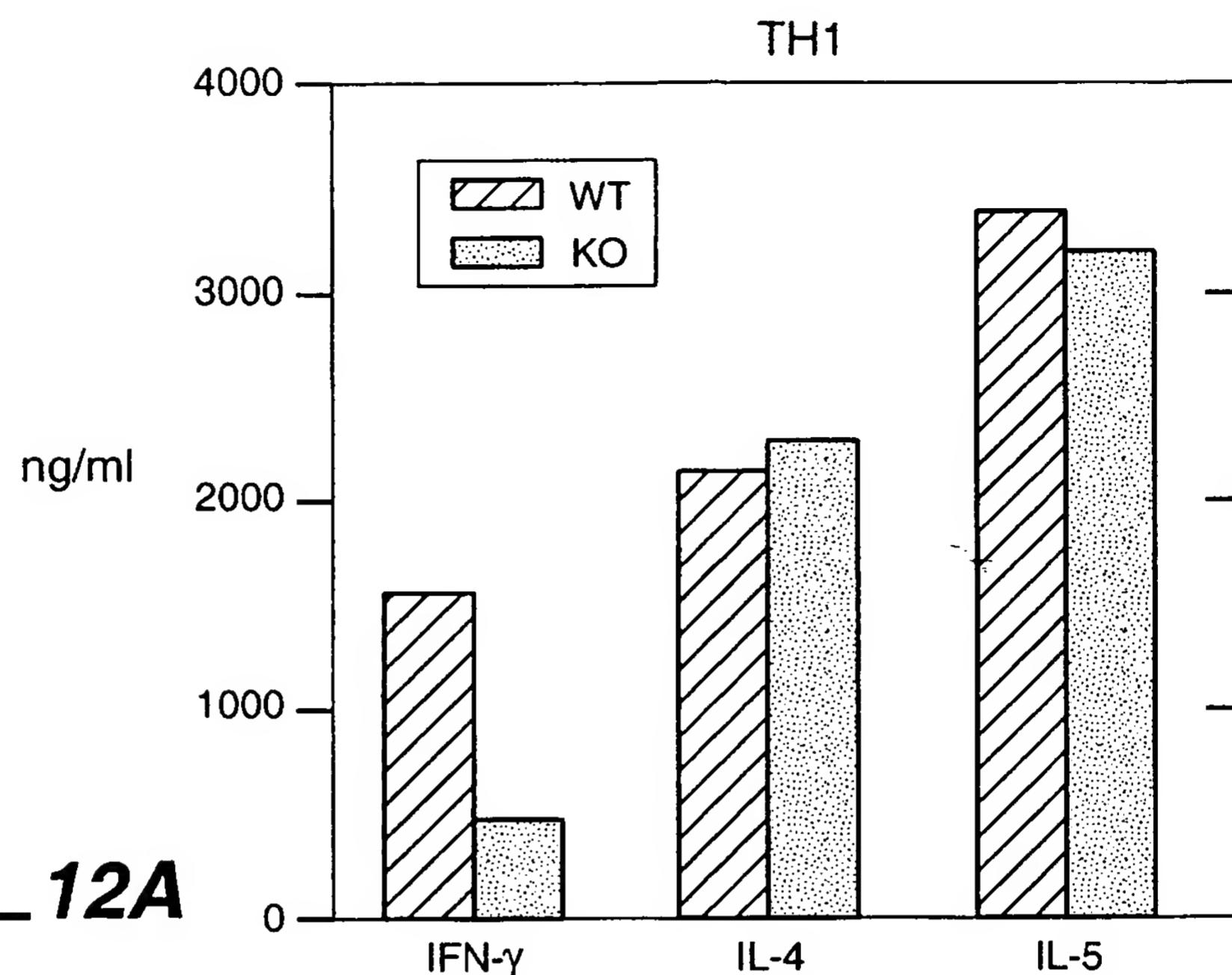


FIG._ 12A

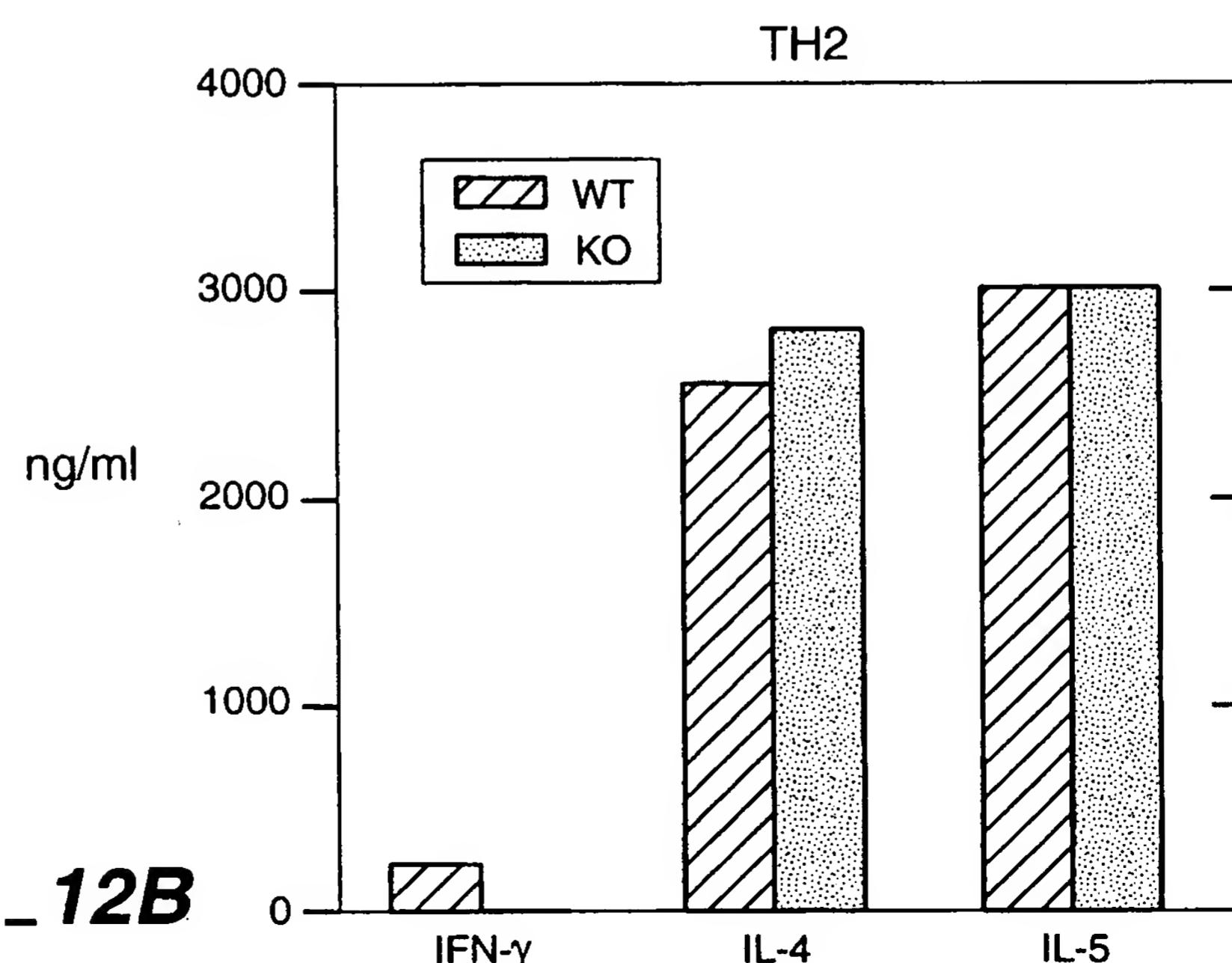
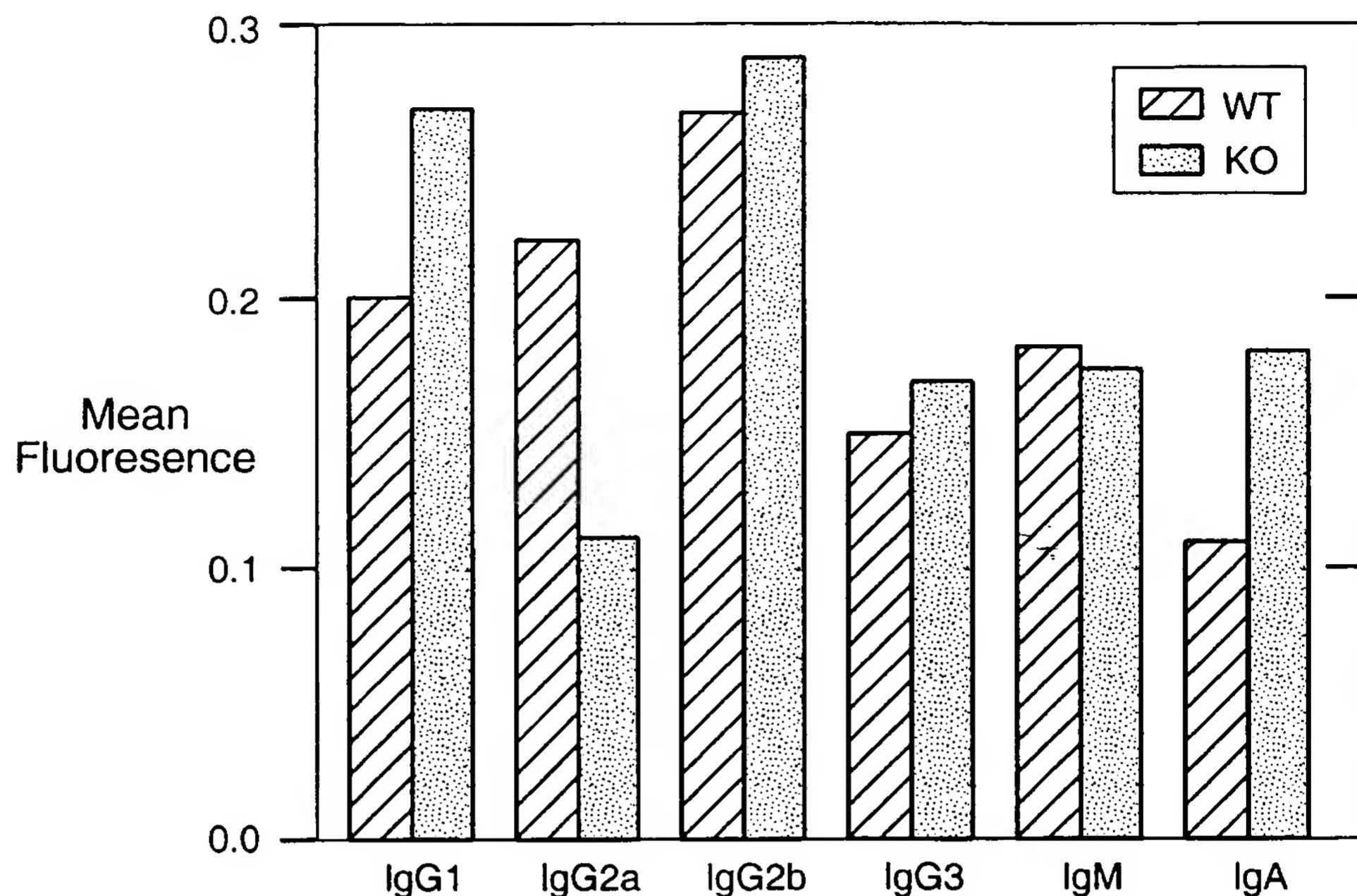
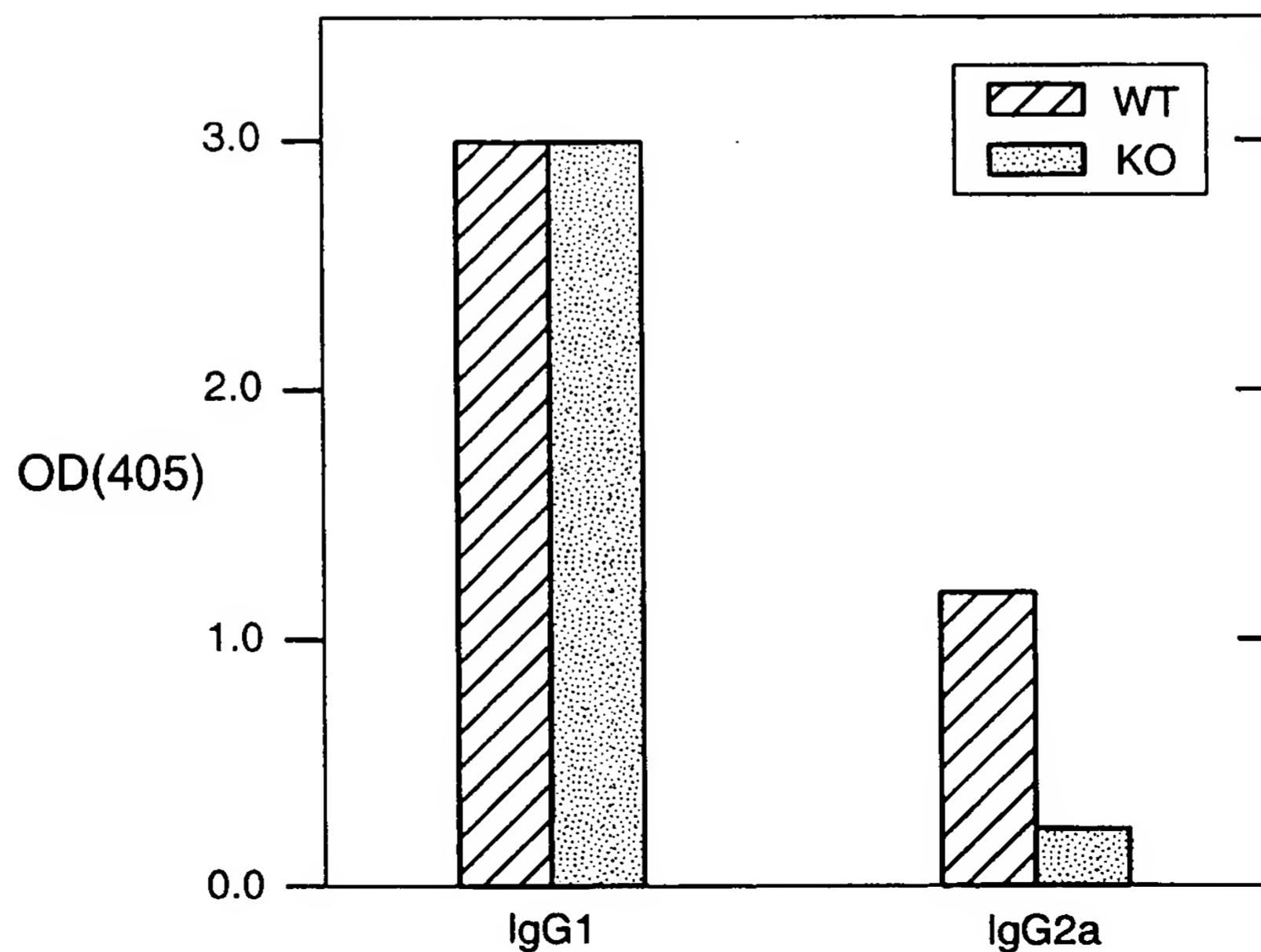


FIG._ 12B

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**FIG._13****FIG._14**

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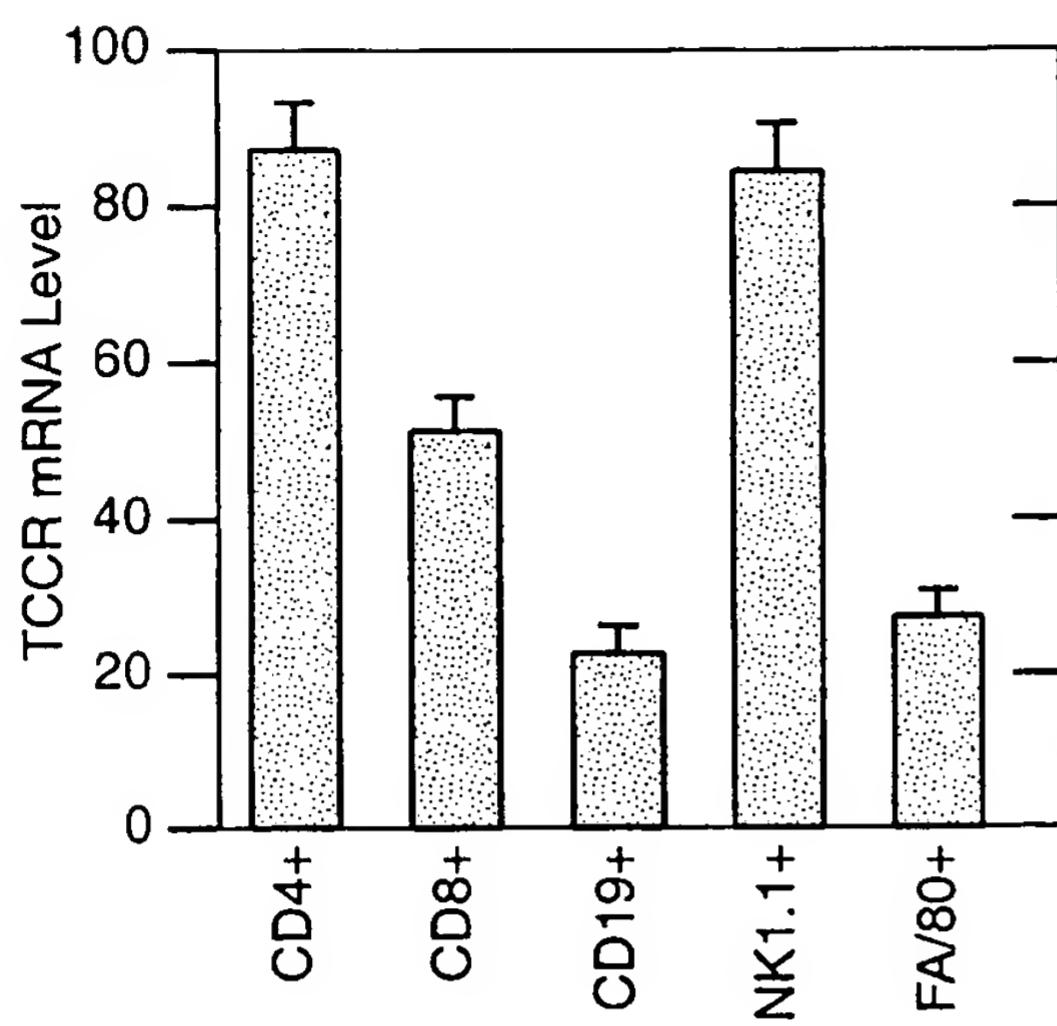


FIG._ 15A

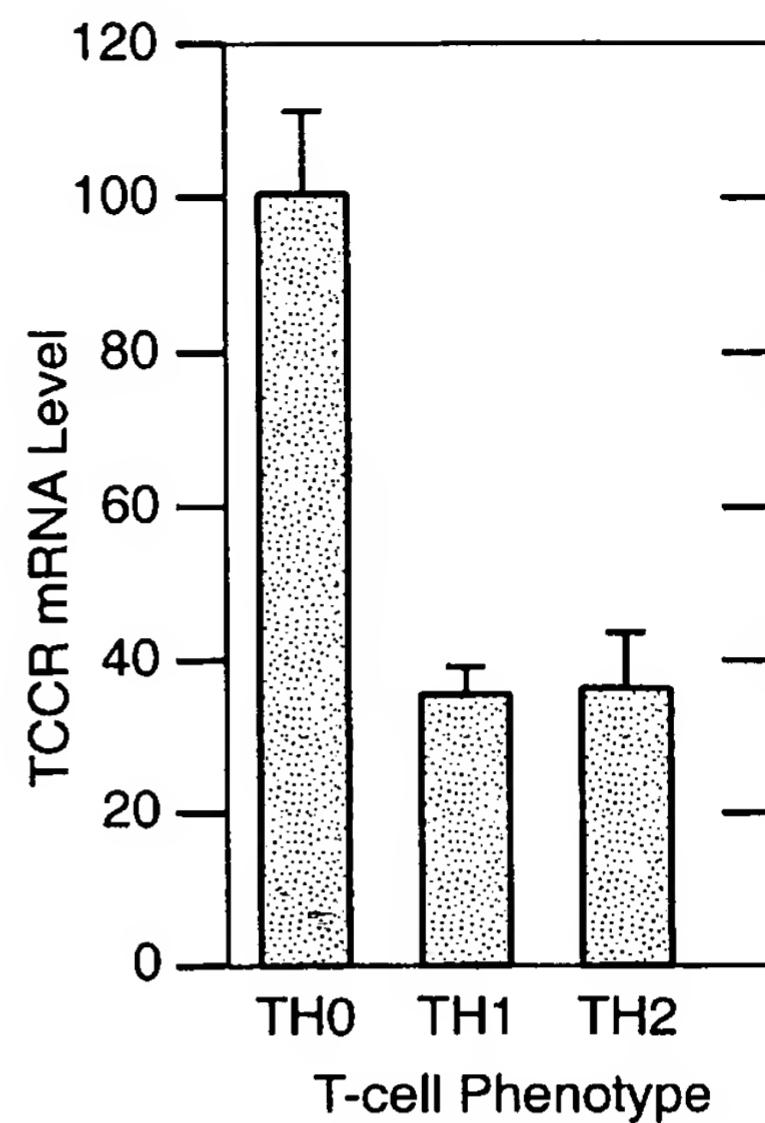


FIG._ 15B

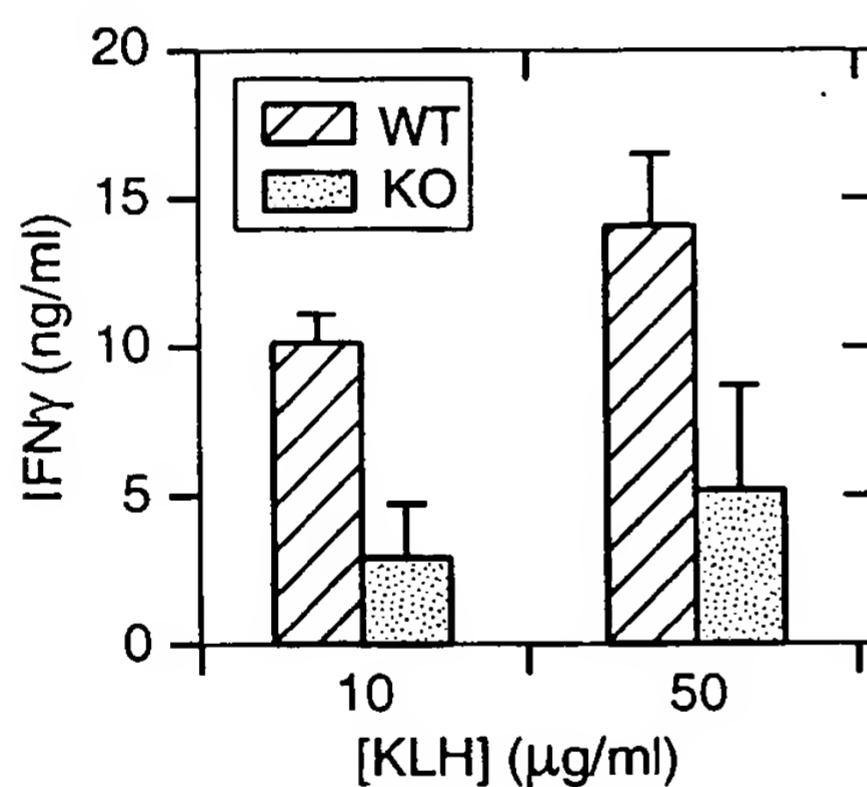


FIG._ 16A

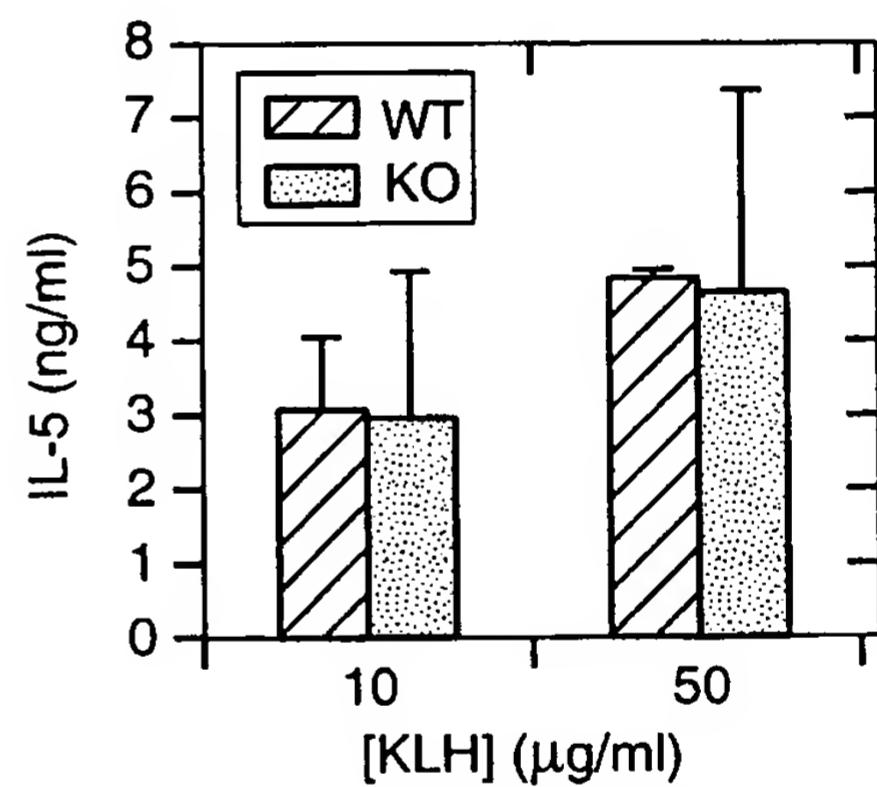


FIG._ 16C

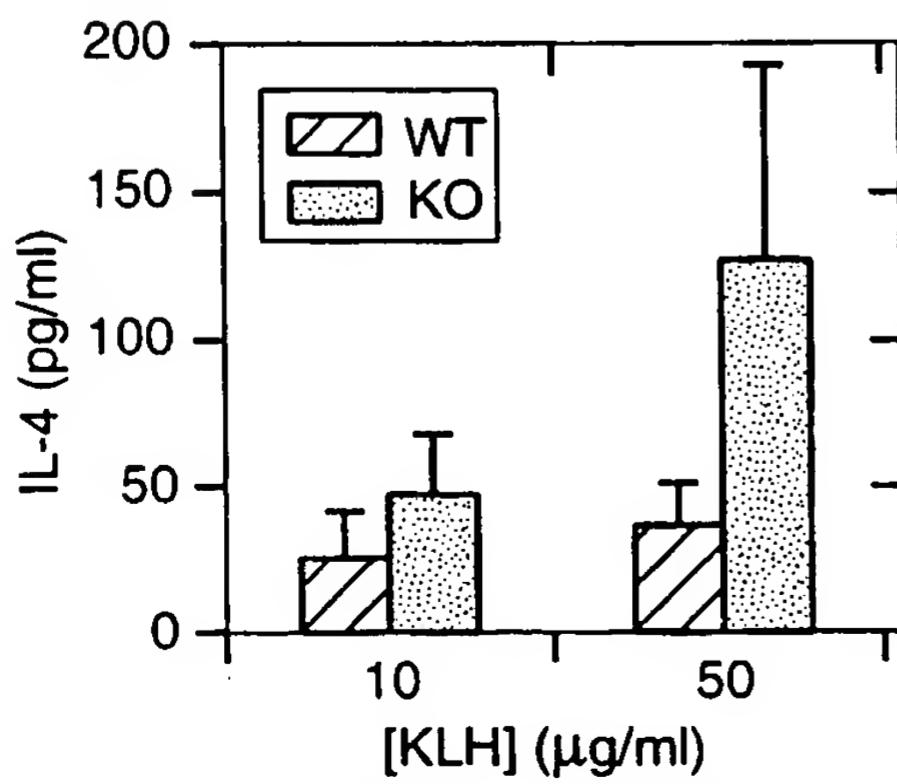


FIG._ 16B

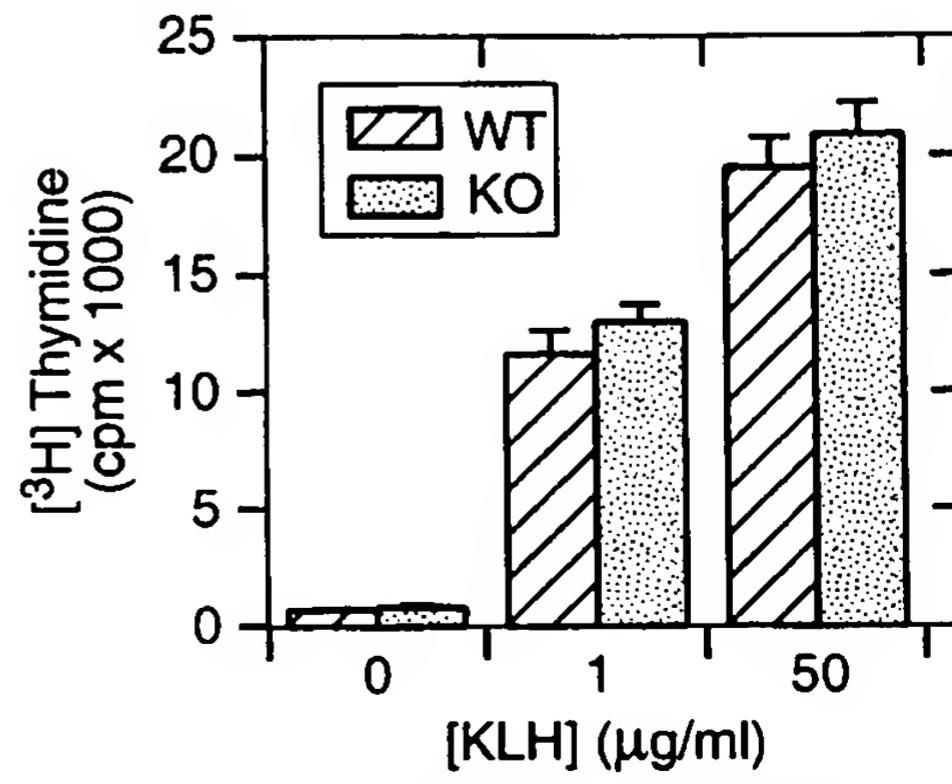


FIG._ 16D

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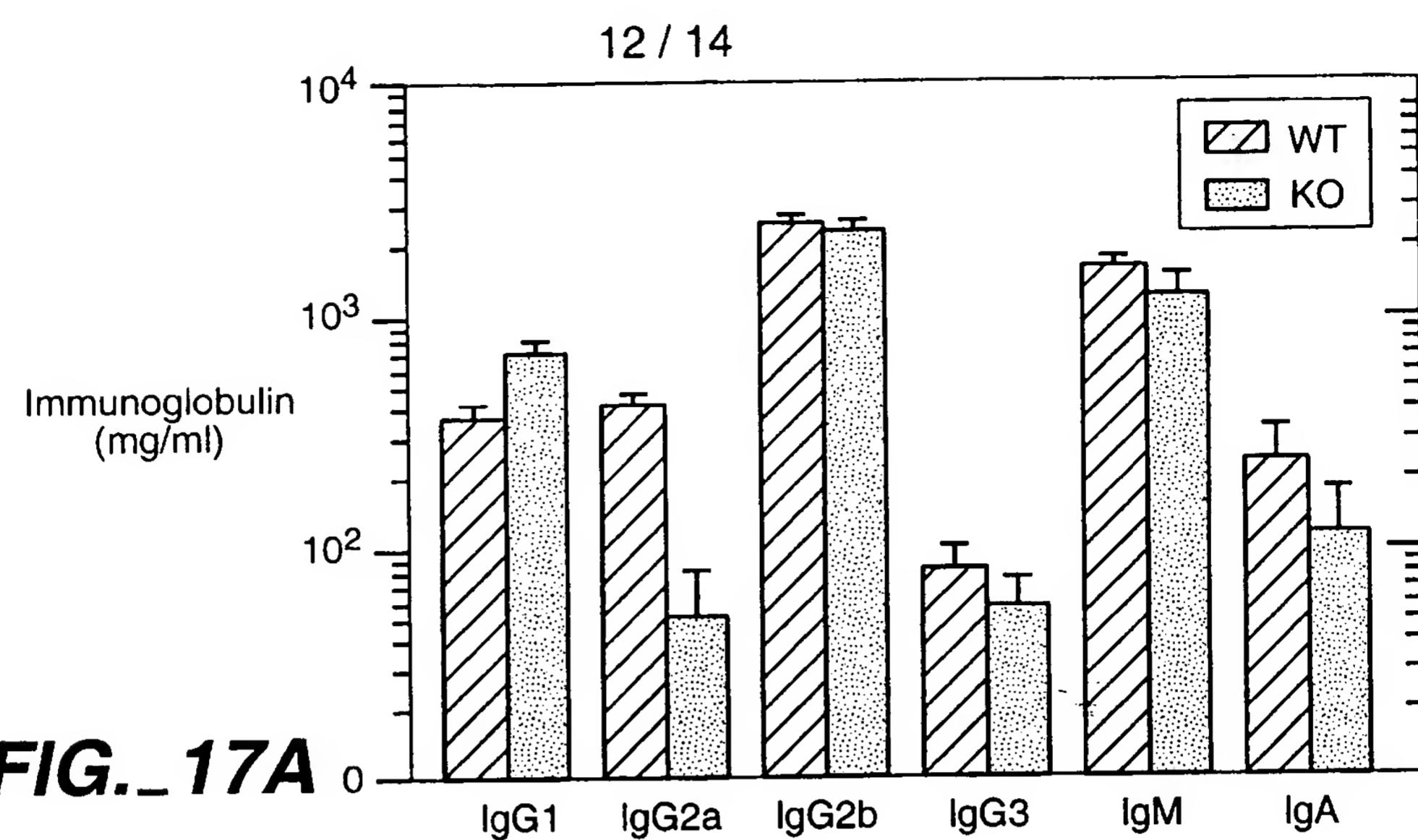


FIG._ 17A

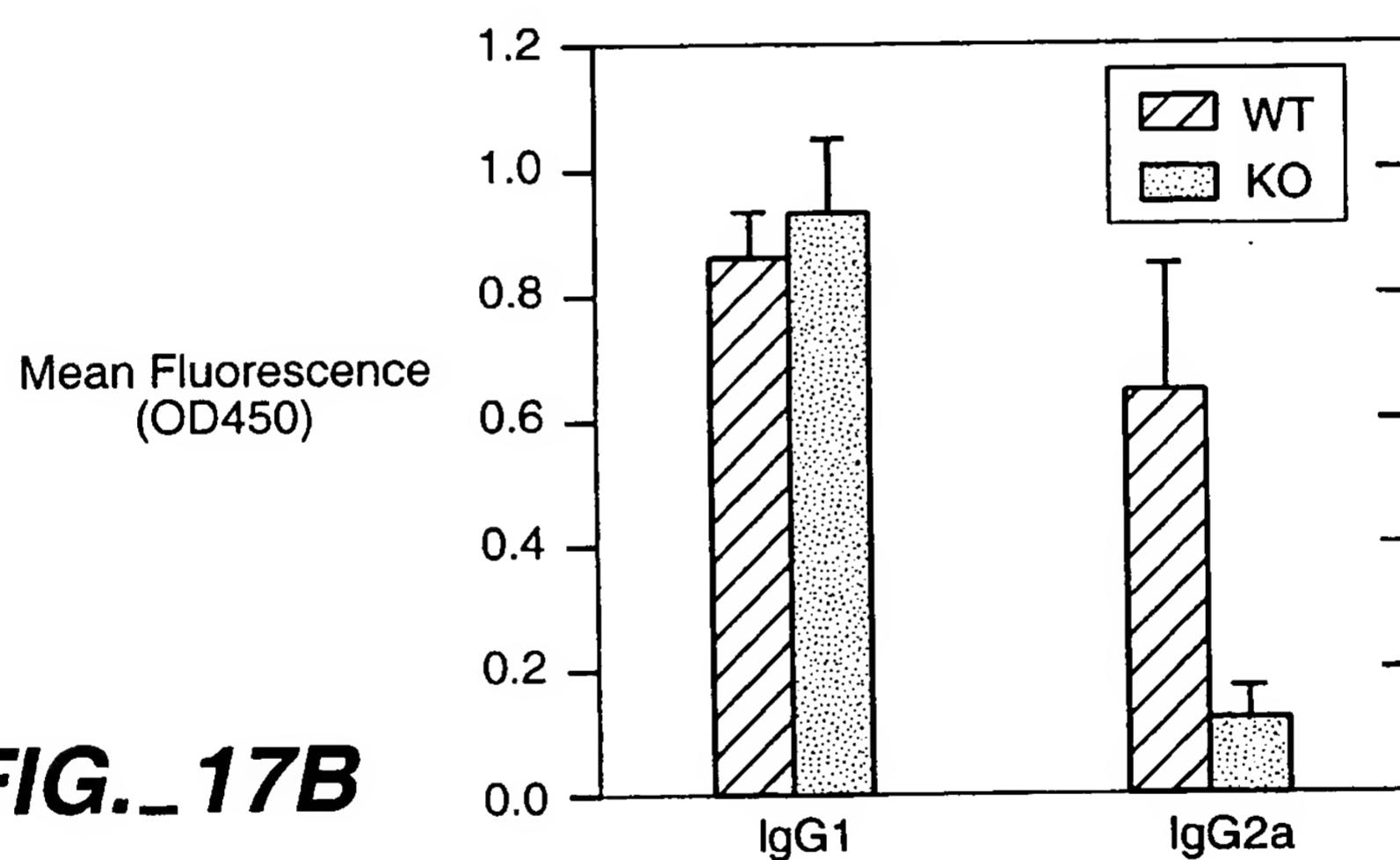


FIG._ 17B

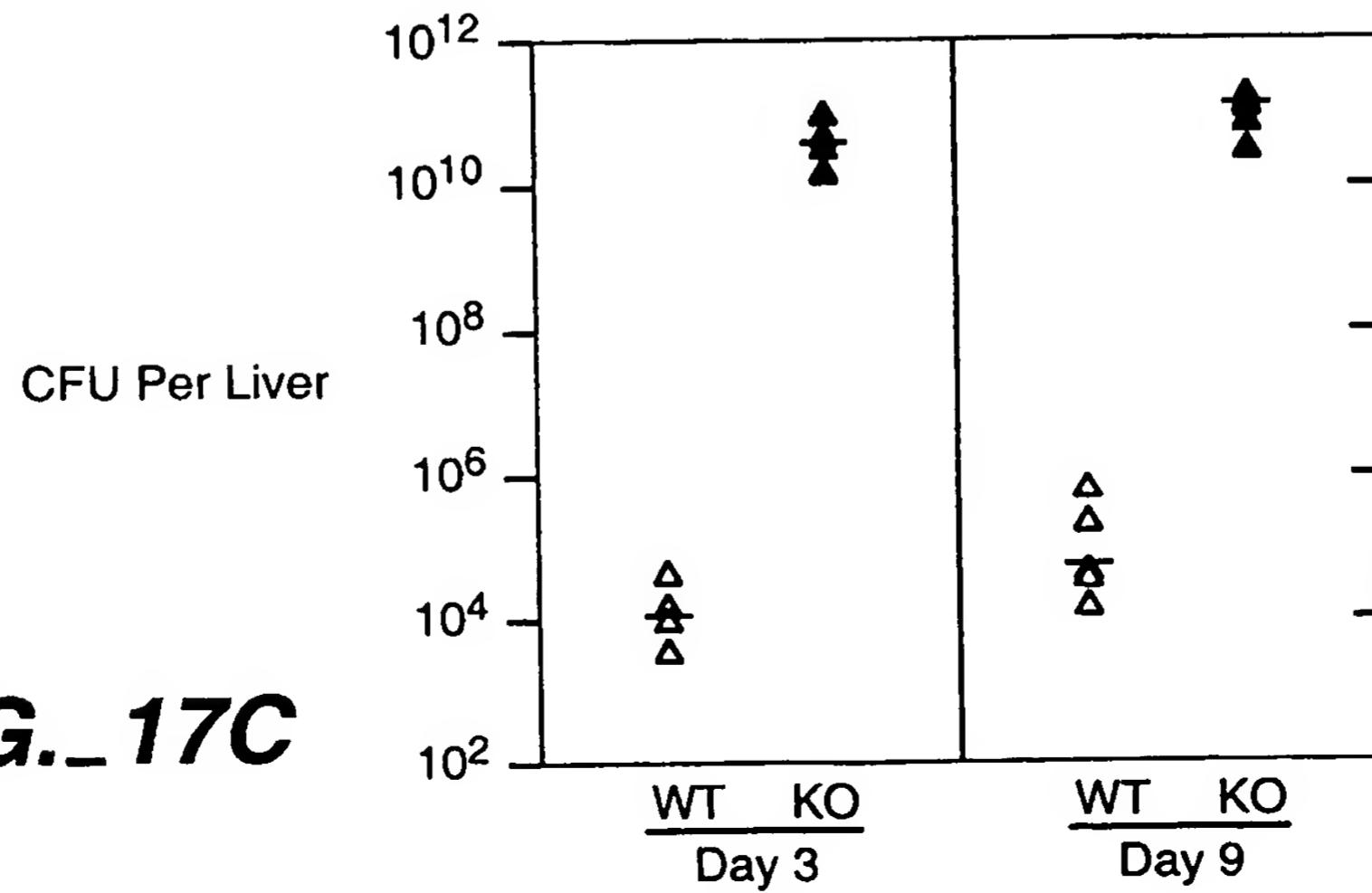


FIG._ 17C

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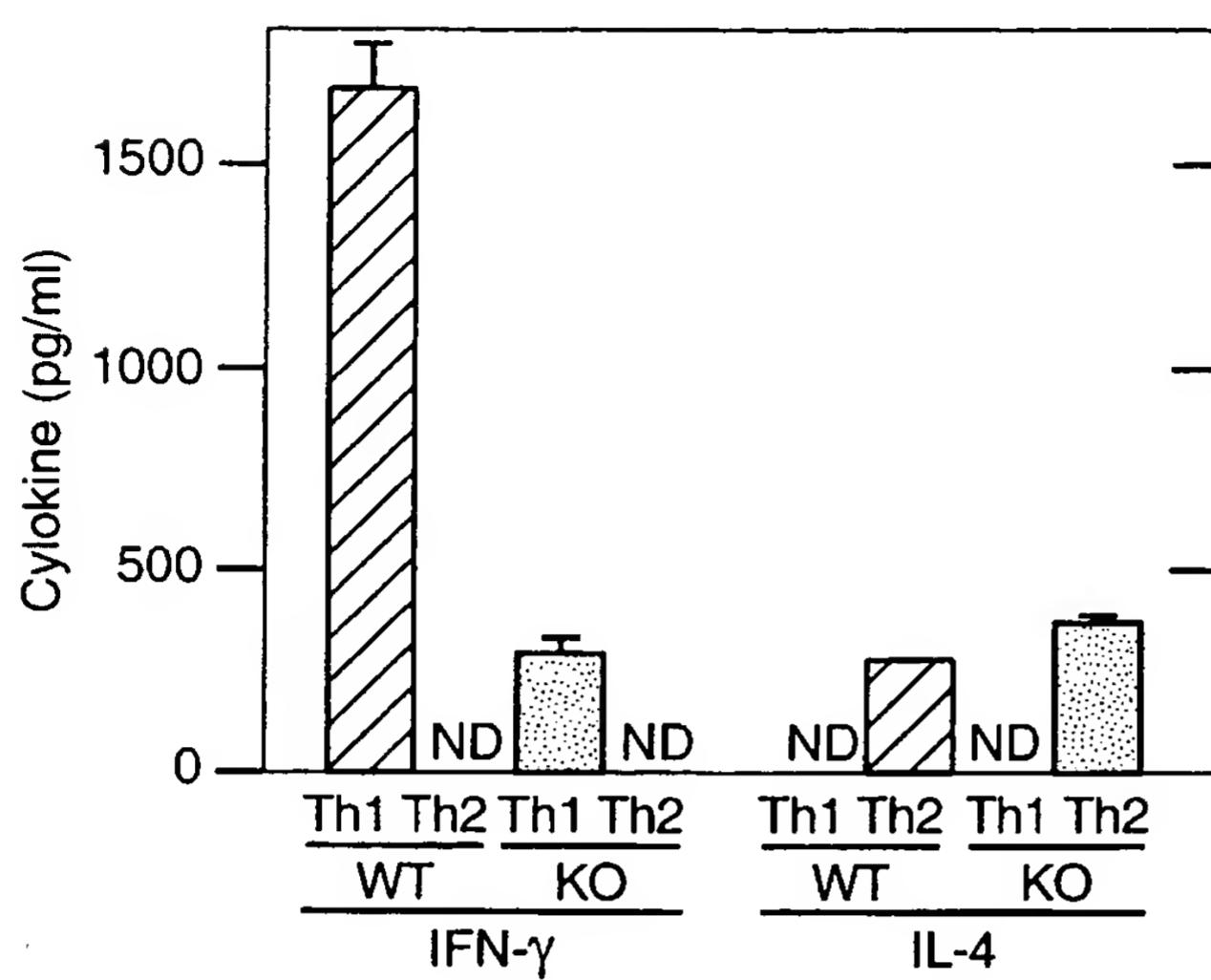


FIG._18A

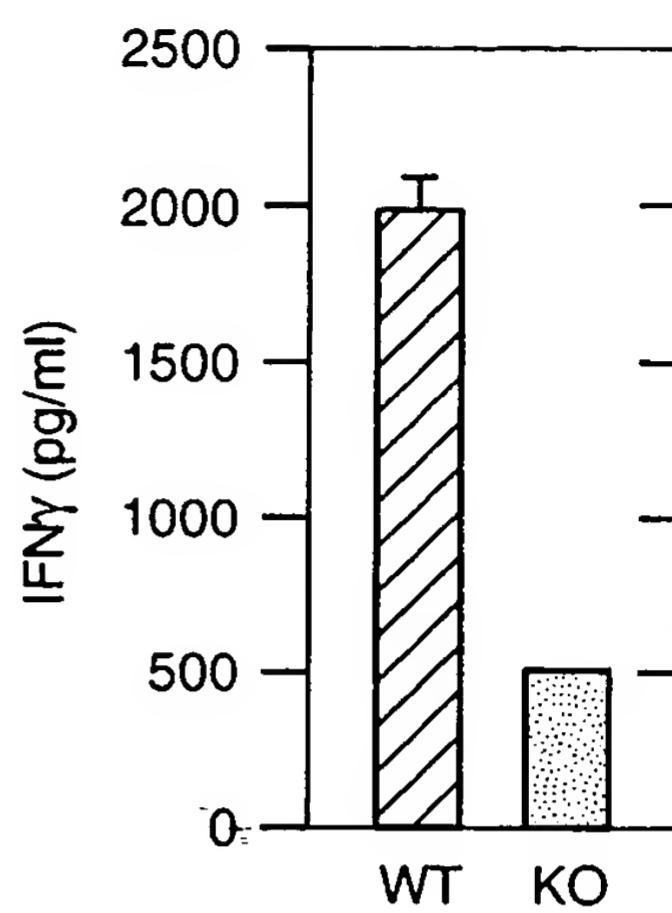


FIG._18B

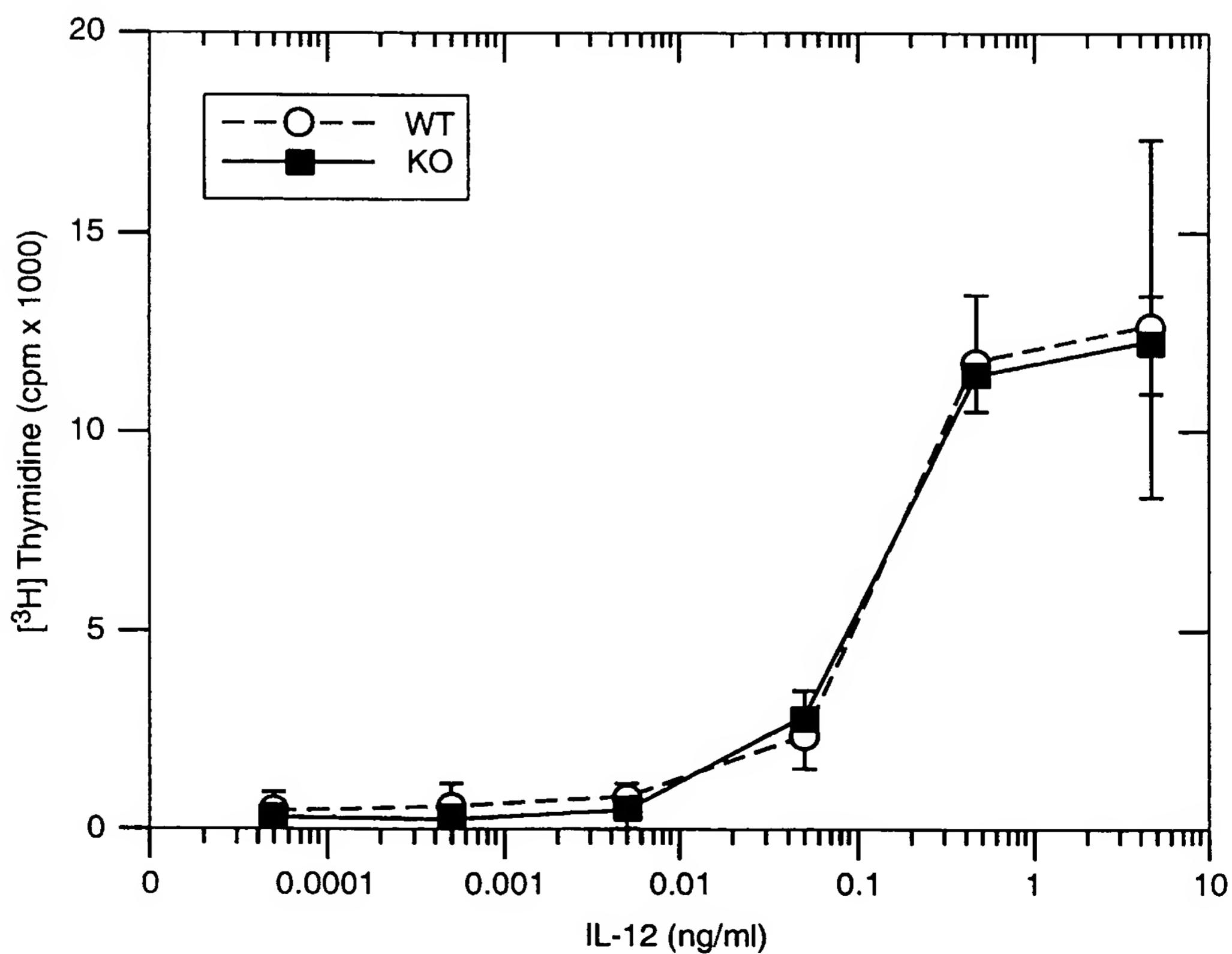
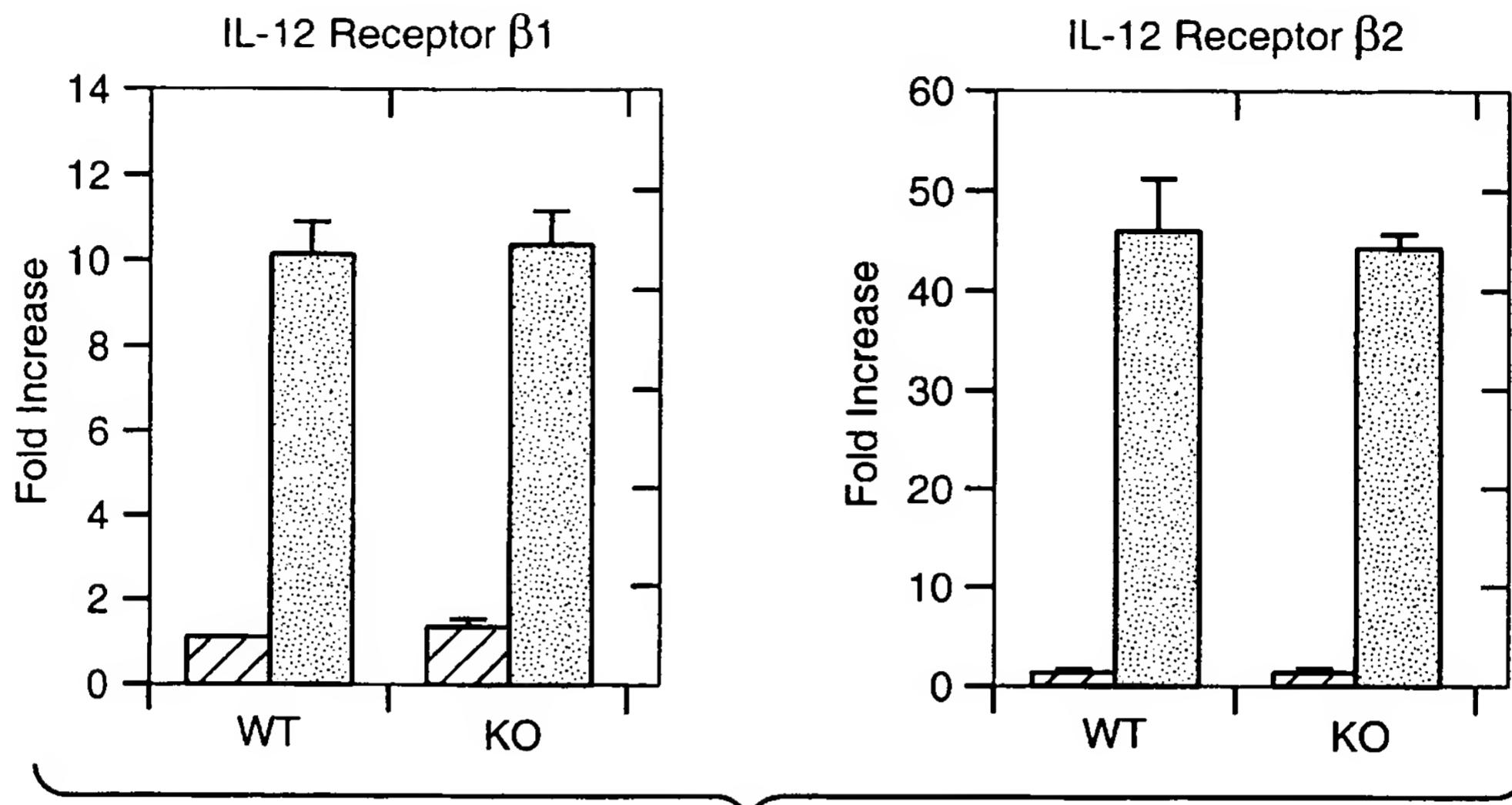


FIG._18C

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***FIG._18D***

| <u>Primer / Probe</u> | <u>Sequence</u> | <u>SEQ ID NO:</u> |
|-------------------------|--------------------------|-------------------|
| mTCCR, sense, Taqman | TGGTCTCTCCTGGAACAGC | 5 |
| mTCCR, as, Taqman | AGCCAAGCACACCAGAGACA | 6 |
| mTCCR, Taqman probe | CAGCTGGGTGCCTCCCACCAA | 7 |
| mRPL19, sense, Taqman | ATCCGCAAGCCTGTGACTGT | 8 |
| mRPL19, as, Taqman | TCGGGCCAGGGTGTTTTT | 9 |
| mRPL19, Taqman probe | TTCCCGGGCTCGTTGCCG | 10 |
| miL12Rb1, sense, Taqman | TCGCGTCTCTGGGAAGCT | 11 |
| miL12Rb1, as, Taqman | TTTAAGCCAATGTATCCGAGACTG | 12 |
| miL12Rb1, Taqman probe | CGCCAGCGTCCTCCTCGTGG | 13 |
| miL12Rb2, sense, Taqman | CAAGCATTGCATCGCTATCA | 14 |
| miL12Rb2, as, Taqman | AATGCCTTTGCCGGAAGT | 15 |
| miL12Rb2, Taqman probe | ACGAATTGAGAACGTGCCACCGT | 16 |

FIG._19